

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101 628,525A
Source: TFW16
Date Processed by STIC: 7-6-05

ENTERED



IFW16

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/628,525A

DATE: 07/06/2005
 TIME: 12:29:49

Input Set : A:\1505604.app
 Output Set: N:\CRF4\07062005\J628525A.raw

3 <110> APPLICANT: KEELING, PETER
 4 GAUN, HANPLING
 6 <120> TITLE OF INVENTION: STARCH ENCAPSULATION
 8 <130> FILE REFERENCE: 15056-04
 10 <140> CURRENT APPLICATION NUMBER: 10/628,525A
 11 <141> CURRENT FILING DATE: 2003-07-28
 13 <150> PRIOR APPLICATION NUMBER: 09/625,406
 14 <151> PRIOR FILING DATE: 2000-07-25
 16 <150> PRIOR APPLICATION NUMBER: 08/941,445
 17 <151> PRIOR FILING DATE: 1997-09-30
 19 <150> PRIOR APPLICATION NUMBER: 60/026,855
 20 <151> PRIOR FILING DATE: 1996-09-30
 22 <160> NUMBER OF SEQ ID NOS: 40
 24 <170> SOFTWARE: PatentIn Ver. 3.3
 26 <210> SEQ ID NO: 1
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 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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 40 <211> LENGTH: 36
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 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
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 65 <210> SEQ ID NO: 4
 66 <211> LENGTH: 4800

(pg. 6)

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Input Set : A:\1505604.app
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75 <221> NAME/KEY: CDS
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79 <221> NAME/KEY: CDS
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83 <221> NAME/KEY: CDS
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95 <221> NAME/KEY: CDS
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127 tgggtctcg tctccgtgtgc ttcctggta gcttgtgttag tggagctgac atggtctgag 180
129 caggcttaaa atttgctcgt agacgaggag taccacgaca gcacgttgcg gatttctctg 240
131 cctgtgaagt gcaacgtcta ggattgtcac acgccttggc cgcgtcgcgt cgcgtcgcgt 300
133 cgtatgcgggtg gtgagcagag cagcaacagc tggcgccccc aacgttgct tccgtgtctt 360
135 cgtcgtacgt acgcgcgcgc cggggacacg cagcagagag cggagagcga gccgtgcacg 420

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137 gggaggtggt gtggaagtgg agccgcgcgc ccggccgccc gcgcgggtg ggcaacccaa 480
 139 aagtacccac gacaagcgaa gcgcggcaag cgatccaagc tccggAACGC aacagcatgc 540
 141 gtcgcgtcgg agagcagcc acaaggcagcc gagaaccgaa ccgggtggcg acgcgtcatg 600
 143 ggacggacgc gggcgacgct tccaaacggg ccacgtacgc cggcgtgtgc gtgcgtgcag 660
 145 acgacaagcc aaggcgaggc agcccccgat cggaaaagcg ttttggcg gagegctggc 720
 147 gtgcgggtca gtcgtggtg cgcaagtgcgg gggggAACGG gtatcggtgg gggcgccggc 780
 149 ggaggagagc gtggcgaggc ccgagagcag cgcgcggccg ggtcacgcaa cgcgcggcc 840
 151 gtactgccct cccctccgc gcgcgttaga aataccgagg cctggaccgg gggggggccc 900
 153 cgtcacatcc atccatcgac cgatcgatcg ccacagccaa caccacccgc cgaggcgacg 960
 155 cgacagccgc caggaggaag gaataaaactc actgccagcc agtgaagggg gagaagtgt 1020
 157 ctgtccgtc gaccagtgcg cgcacccgc ggcagggtg ctcatctcg cgacgaccag 1080
 159 gttctgttcc gttccgatcc gatccgatcc tgtcctttag tttcggtccag atccctggc 1140
 161 gatatctcggt gttttagatcg ccagggttctt cgaacctaaa tctgtccgt cacacgttt 1200
 163 ttctctctct cctacgcagt ggattaatcg gcatggcgcc tctggccacg tcgcagctcg 1260
 165 tcgcaacgcgc cggccgcctg gcgcgtcccg acgcgtccac gttccgcgc ggcgcgcgc 1320
 167 agggcctgag gggggcccg gcgtcggcg cggccgacac gctcagcatg cggaccagcg 1380
 169 cgcgcgcgc gcccaggcac cagcagcagg cgcgcgcgg gggcagggtc ccgtcgctcg 1440
 171 tcgtgtgc gcc agc gcc ggc atg aac gtc gtc ttc gtc ggc gcc gag atg 1490
 172 Ala Ser Ala Gly Met Asn Val Val Phe Val Gly Ala Glu Met
 173 1 5 10
 175 gcg ccg tgg agc aag acc ggc ggc ctc ggc gac gtc ctc ggc ggc ctg 1538
 176 Ala Pro Trp Ser Lys Thr Gly Gly Leu Gly Asp Val Leu Gly Gly Leu
 177 15 20 25 30
 179 ccg ccg gcc atg gcc gtaagcgccgc gcacccgagac atgcattccgt tggatcgctg 1593
 180 Pro Pro Ala Met Ala
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 183 ctcttcgtc ctcttgcgc gtgcgtatcg catgttttc ctcttgcgtt gtgttcgtgt 1653
 185 atgtgacgtg tttgttcggg catgcgtca g ggc aac ggg cac cgt gtc atg 1705
 186 Ala Asn Gly His Arg Val Met
 187 40
 188 gtc gtc tct ccc cgc tac gac cag tac aag gac gcc tgg gac acc agc 1753
 189 Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp Asp Thr Ser
 190 45 50 55
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 192 gtc gtg tcc gag gtacggccac cgagaccaga ttcaagatcac agtcacacac 1805
 193 Val Val Ser Glu
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 197 accgtcatat gaaccttct ctgtctgtat gcctgcaact gcaaattgtat gcag atc 1862
 198 Ile
 199 aag atg gga gac ggg tac gag acg gtc agg ttc ttc cac tgc tac aag 1910
 200 Lys Met Gly Asp Gly Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys
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215 Glu Lys Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln
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 218 ctg cgg ttc agc ctg cta tgc cag gtcaggatgg cttggacta caacttcata 2174
 219 Leu Arg Phe Ser Leu Leu Cys Gln
 220 120 125
 222 tcacatgtat gcagcagtat acactgtat gaaatgcattt ctgttctgca g gca gca 2231
 223 Ala Ala
 225 ctt gaa gct cca agg atc ctg agc ctc aac aac aac cca tac ttc tcc 2279
 226 Leu Glu Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser
 227 130 135 140
 229 gga cca tac ggtaagagtt gcagtcttcg tatatatatc tgttgagctc 2328
 230 Gly Pro Tyr
 231 145
 233 gagaatcttc acaggaagcg gcccatcaga cggactgtca ttttacactg actactgctg 2388
 235 ctgctcttcg tccatccata caa ggg gag gac gtc gtg ttc gtc tgc aac gac 2441
 236 Gly Glu Asp Val Val Phe Val Cys Asn Asp
 237 150 155
 239 tgg cac acc ggc cct ctc tcg tgc tac ctc aag agc aac tac cag tcc 2489
 240 Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys Ser Asn Tyr Gln Ser
 241 160 165 170
 243 cac ggc atc tac agg gac gca aag gttgccttctt ctgaactgaa caacggcg 2543
 244 His Gly Ile Tyr Arg Asp Ala Lys
 245 175 180
 247 ttccgttctcc atgctcgat atacctcgat tggtagtggt ggtgccttc tgagaaacta 2603
 249 actgaaaactg actgcattgtc tgtctgacca tcttcacgta ctaccag acc gct ttc 2659
 250 Thr Ala Phe
 252 tgc atc cac aac atc tcc tac cag ggc cgg ttc gcc ttc tcc gac tac 2707
 253 Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
 254 185 190 195
 256 ccg gag ctg aac ctc ccg gag aga ttc aag tcg tcc ttc gat ttc atc 2755
 257 Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
 258 200 205 210 215
 260 gac ggg tctgtttcc tgcgtgcattt tgaacattca tgaatggtaa cccacaactg 2811
 261 Asp Gly
 263 ttccgttctt gctgggtcat tatctgaccc gattgcattt ttgcagg tac gag aag 2867
 264 Tyr Glu Lys
 265 220
 267 ccc gtg gaa ggc cgg aag atc aac tgg atg aag gcc ggg atc ctc gag 2915
 268 Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys Ala Gly Ile Leu Glu
 269 225 230 235
 271 gcc gac agg gtc ctc acc gtc agc ccc tac tac gcc gag gag ctc atc 2963
 272 Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile
 273 240 245 250
 275 tcc ggc atc gcc agg ggc tgc gag ctc gac aac atc atg cgc ctc acc 3011
 276 Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr
 277 255 260 265
 279 ggc atc acc ggc atc gtc aac ggc atg gac gtc agc gag tgg gac ccc 3059
 280 Gly Ile Thr Gly Ile Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro
 281 270 275 280

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287	gtgagctggc	tagctctgat	tctgctgcct	ggtcctcctg	ctcatcatgc	tggttcggtta									3161			
289	ctgacgcggc	aagtgtacgt	acgtgcgtgc	gacggtggtg	tccggttcag	gcc	gtg								3217			
290													Ala	Val				
291													300					
293	gag	gcc	aag	gcg	ctg	aac	aag	gag	gcg	ctg	cag	gcg	gag	gtc	ggg	3265		
294	Glu	Ala	Lys	Ala	Leu	Asn	Lys	Glu	Ala	Leu	Gln	Ala	Glu	Val	Gly	Leu		
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297	ccg	gtg	gac	cgg	aac	atc	ccg	ctg	gtg	gcg	ttc	atc	ggc	agg	ctg	3313		
298	Pro	Val	Asp	Arg	Asn	Ile	Pro	Leu	Val	Ala	Phe	Ile	Gly	Arg	Leu	Glu		
299		320				325							330					
301	gag	cag	aag	ggc	ccc	gac	gtc	atg	gcg	gcc	atc	ccg	cag	ctc	atg	3361		
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303		335			340			345										
305	gag	atg	gtg	gag	gac	gtg	cag	atc	gtt	ctg	ctg	gtacgtgtgc	gccggccgccc		3414			
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312				Gly	Thr	Gly	Lys	Lys	Phe	Glu	Arg	Met	Leu	Met				
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317		375			380			385										
319	aac	gcg	gcg	ctg	cac	cac	atc	atg	gcc	ggc	gac	gtg	ctc	gcc		3621		
320	Asn	Ala	Ala	Leu	Ala	His	His	Ile	Met	Ala	Gly	Ala	Asp	Val	Leu	Ala		
321		390			395			400										
323	gtc	acc	agc	cgc	ttc	gag	ccc	tgc	ggc	ctc	atc	cag	ctg	cag	ggg	3669		
324	Val	Thr	Ser	Arg	Phe	Gl	Pro	Cys	Gly	Leu	Ile	Gln	Leu	Gln	Gly	Met		
325		405			410			415										
327	cga	tac	gga	acg	gtacgagaga	aaaaaaaaat	cctgaatcct	gacgagaggg							3721			
328	Arg	Tyr	Gly	Thr														
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331	acagagacag	attatgaatg	tttcatcgat	tttgaatttgc	tatcgatgt	ctcccgctgc									3781			
333	gactcttgca	g	ccc	tgc	gcc	tgc	gcg	tcc	acc	ggt	gga	ctc	gtc	gac	acc	3831		
334				Pro	Cys	Ala	Cys	Ala	Ser	Thr	Gly	Gly	Leu	Val	Asp	Thr		
335		425			430			435										
337	atc	atc	gaa	ggc	aag	acc	ggg	ttc	cac	atg	ggc	cgc	ctc	agc	gtc	gac	3879	
338	Ile	Ile	Glu	Gly	Lys	Thr	Gly	Phe	His	Met	Gly	Arg	Leu	Ser	Val	Asp		
339		440			445			450										
341	gtaaggcttag	ctctgccatg	ttttttcttc	tttttttctc	tatgtatgtt	tgaatcagca										3939		
343	ccggccgttct	tgtttcgatc	tgcgtatcttc	ttccccag	tgt	aac	gtc	gtg	gag	ccg						3994		
344													Cys	Asn	Val	Val	Glu	Pro
345													455					
347	gcg	gac	gtc	aag	aag	gtg	gcc	acc	aca	ttg	cag	cgc	gcc	atc	aag	gtg	4042	
348	Ala	Asp	Val	Lys	Lys	Val	Ala	Thr	Thr	Leu	Gln	Arg	Ala	Ile	Lys	Val		
349		460			465			470										

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:37; Xaa Pos. 17

Seq#:39; Xaa Pos. 2

VERIFICATION SUMMARY DATE: 07/06/2005
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L:3057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:16
L:3093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0